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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 04:39:04 ; Search time 211.95 Seconds

(without alignments)  
3815.365 Million cell updates/sec

Title: US-09-525-361A-23  
Perfect score: 471

Sequence: 1 cttgaagatttctctg.....aactatgagcagctaacaat 471

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_032802:\*

1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
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13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469.4	99.7	471	21	AA54120
2	469.4	99.7	471	22	AA54120
3	448.4	95.2	480	20	AA54120
4	448.4	95.2	480	21	AA54120
5	448.4	95.2	480	22	AA54120
6	448.4	95.2	489	20	AA54120
7	448.4	95.2	489	21	AA54120
8	448.4	95.2	578	21	AA54120
9	448.4	95.2	578	22	AA54120

10	447	94.9	482	19	AA531992	BS106 polynucleot
11	447	94.9	482	20	AA53581	BS106 consensus po
12	446.8	94.9	553	19	AA531993	BS106 polynucleot
13	446.8	94.9	553	20	AA53582	BS106 consensus po
14	446.4	94.8	544	21	AA521765	Human breast speci
15	446.2	94.7	472	22	AA521765	Human breast speci
16	446.2	94.7	472	22	AA521765	Human breast speci
17	443	94.1	471	21	AA521765	Human breast speci
18	443	94.1	471	21	AA521765	Human breast speci
19	442.2	93.9	488	22	AA521765	Human breast speci
20	442.2	93.9	488	22	AA521765	Human breast speci
21	300.8	63.9	308	19	AA531990	Human angiotensin
22	300.8	63.9	308	20	AA535579	Human angiotensin
23	300.8	63.9	308	22	AA535579	Human angiotensin
24	298.8	63.4	501	23	AA587721	Human breast cance
25	298.8	63.4	501	23	AA587721	Human breast cance
26	271.4	57.6	273	21	AA54121	Human breast cance
27	271.4	57.6	273	21	AA54121	Human breast cance
28	255.6	54.3	264	22	AA53399	Human breast cance
29	247.2	52.5	291	22	AA53399	Human breast cance
30	202.8	43.1	229	19	AA531989	Human breast cance
31	202.8	43.1	229	20	AA535578	Human breast cance
32	186.4	39.6	201	22	AA535578	Human breast cance
33	181.4	38.5	197	19	AA531991	Human breast cance
34	181.4	38.5	197	20	AA535580	Human breast cance
35	181.4	38.5	197	22	AA535580	Human breast cance
36	94	20.0	660	23	AA587720	Human breast cance
37	70.2	14.9	397	20	AA587720	Human breast cance
38	65.4	13.9	477	21	AA541307	Human breast cance
39	65	13.8	234	16	AA54832	Human breast cance
40	64.8	13.8	1326	23	AA581104	Human breast cance
41	64.8	13.8	3376	16	AA575166	Human breast cance
42	64.6	13.7	203	19	AA530271	Human breast cance
43	64.6	13.7	203	19	AA530271	Human breast cance
44	64.6	13.7	1037	21	AA539242	Human breast cance
45	64.6	13.7	1472	21	AA539241	Human breast cance

## ALIGNMENTS

RESULT 1	AA54120	standard; DNA: 471 BP.
ID	AA54120	
AC	AA54120	
XX		
DT	08-FEB-2001	(first entry)
DE	Breast cancer protein BCL1 coding sequence.	
KW	Breast cancer; diagnosis; prognosis; detection; screening; antibody; oestrogen receptor; anti-oestrogen; immune response; lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCL1; BCN2; BCN3; BCQ2; BCX2; BCX3; BCA2; BCR2; BCT7; BCY3; human; ds.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	47..319
FT		/*tag= a
FT		/product= BCL1 protein
XX		
PN	WO200055629-A2.	
XX		
PD	21-SEP-2000.	
XX		
PF	15-MAR-2000; 2000WO-US06952.	
XX		
PR	15-MAR-1999; 99US-0268665.	
PR	12-NOV-1999; 99US-0439878.	
PR	12-NOV-1999; 99US-0440370.	
PR	15-NOV-1999; 99US-0440493.	